

AGCATCCTGA	GTAATGAGTG	GCCTGGGCGG	GAGCAGGCGA	GGTGGCCGGA	GCCGTGTGGA	60
CCAGGAGGAG	CGCTTTCCAC	AGGGCCTGTG	GACGGGGGTG	GCTATGAGAT	GCTGCCCCGA	120
AGAGCAGTAC	TGGGATCCTC	TGCTGGGTAC	CTGCATGTCC	TGCAAAACCA	TTTGCAACCA	180
TCAGAGCCAG	CGCACCTGTG	CAGCCTTCTG	CAGGTCACCT	AGCTGCCGCA	AGGAGCAACG	240
CAAGTTCTAT	GACCATCTCC	TGAGGGACTG	CATCAGCTGT	GCCTCCATCT	GTGGACAGCA	300
CCCTAAGCAA	TGTGCATACT	TCTGTGAGAA	CAAGCTCAGG	AGCCCAAGTA	ACCTTCCACC	360
AGAGCTCAGG	AGACAGCGGA	GTGGAGAACT	TGAAAACAAT	TCAGACAACCT	CGGGAAGGTA	420
CCAAGGATTG	GAGCACAGAG	GCTCAGAAGC	AAGTCCAGCT	CTCCCGGGGC	TGAAGCTGAG	480
TGCAGATCAG	GTGGCCCTGG	TCTACAGCAC	GCTGGGGCTC	TGCCCTGTGTG	CCGTCTCTGTG	540
CTGCTTCTGT	GTGGCGGTGG	CCTGCTTCTT	CAAGAAGAGG	GGGGATCCCT	GCTCTGCCCA	600
GCCCCGCTCA	AGGCCCCGTC	AAAGTCCGGC	CAAGTCTTCC	CAGGATCACT	CGATGGAAGC	660
CGGCAGCCCT	GTGAGCACAT	CCCCGAGGCC	AGTGGAGACC	TGCAGCTTCT	GCTTCCCTGA	720
GTGCAGGGCG	CCCAAGCAGG	AGAGCGCAGT	CACGCCTGGG	ACCCCGGACC	CCACTGTGTG	780
TGGAAGGTGG	GGGTGCCACA	CCAGGACCAC	AGTCTCTCAG	CCTTGCCCAC	ACATCCCCAGA	840
CAGTGGCCTT	GGCATTGTGT	GTGTGCTGCG	CCAGGAGGGG	GGCCCAAGTG	CATAAATGGG	900
GGTCAGGGAG	GGAAAGGAGG	AGGGAGAGAG	ATGGAGAGGA	GGGAGAGAG	AAAGAGAGGT	960
GGGGAGAGGG	GAGAGAGATA	TGAGGAGAGA	GAGACAGAGG	AGGCAGAAAG	GGAGAGAAAC	1020
AGAGGAGACA	GAGAGGGAGA	GAGAGACAGA	GGGAGAGAGA	GACAGAGGGG	AAGAGAGGCA	1080
GAGAGGGAAA	GAGGCAGAGA	AGGAAAGAGA	CAGGCAGAGA	AGGAGAGAGG	CAGAGAGGGA	1140
GAGAGGCAGA	GAGGGAGAGA	GGCAGAGAGA	CAGAGAGGGA	GAGAGGGACA	GAGAGAGATA	1200
GAGCAGGAGG	TGCGGGGCACT	CTGAGTCCCA	GTTCCTCAGT	CAGCTGTAGG	TGCTCATCAC	1260
CTAACCCAC	GTGCAATAAA	GTCCTGTGTC	CTGCTGCTCA	CAGCCCCGGA	GAGCCCCCTCC	1320
TCCTGGAGAA	TAAAACTTTT	GGCAGCTGCC	CTTCTCTAAA	AAAAAAAAAA	AAAAAAA	1377

FIGURE 1A

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
 20 25 30
 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
 35 40 45
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50 55 60
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65 70 75 80
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85 90 95
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
 165 170 175
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
 180 185 190
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
 195 200 205
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
 210 215 220
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
 225 230 235 240
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
 245 250 255
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
 260 265 270
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
 275 280 285
 Gly Gly Pro Gly Ala
 290

FIGURE 1B

AGCAAGTTCA GCCTGGTTAA GTCCAAGCTG AATTCCGGTC AAAGTTCAAG
 TAGTGATATG GATGACTCCA CAGAAAGGGA GCAGTCACGC CTTACTTCTT
 GCCTTAAGAA AAGAGAAGAA ATGAAACTGA AGGAGTGTGT TTCCATCCTC
 CCACGGAAGG AAAGCCCCCTC TGTCCGATCC TCCAAAGACG GAAAGCTGCT
 GGCTGCAACC TTGCTGCTGG CACTGCTGTC TTGCTGCCTC ACGGTGGTGT
 CTTTCTACCA GGTGGCCGCC CTGCAAGGGG ACCTGGCCAG CCTCCGGGCA
 GAGCTGCAGG GCCACCACGC GGAGAAGCTG CCAGCAGGAG CAGGAGCCCC
 CAAGGCCGGC CTGGAGGAAG CTCCAGCTGT CACCGCGGGA CTGAAAATCT
 TTGAACCACC AGCTCCAGGA GAAGGCAACT CCAGTCAGAA CAGCAGAAAT
 AAGCGTGCCG TTCAGGGTCC AGAAGAAACA GTCACTCAAG ACTGCTTGCA
 ACTGATTGCA GACAGTGAAA CACCAACTAT ACAAAAAGGA TCTTACACAT
 TTGTTCCATG GCTTCTCAGC TTTAAAAGGG GAAGTGCCCT AGAAGAAAAA
 GAGAATAAAA TATTGGTCAA AGAAACTGGT TACTTTTTTA TATATGGTCA
 GGTTTTATAT ACTGATAAGA CCTACGCCAT GGGACATCTA ATTCAGAGGA
 AGAAGGTCCA TGCTTTTGGG GATGAATTGA GTCTGGTGAC TTTGTTTCGA
 TGTATTCAAA ATATGCCTGA AACACTACCC AATAATTCTT GCTATTACGC
 TGGCATTGCA AAACCTGGAAG AAGGAGATGA ACTCCAACCT GCAATACCAA
 GAGAAAATGC ACAAATATCA CTGGATGGAG ATGTCACATT TTTTGGTGCA
 TTGAACTGCT TGTGACCTAC TTACACCATG TCTGTAGCTA TTTTCTCCC
 TTTCTCTGTA CCTCTAAGAA GAAAGAATCT AACTGAAAT ACCAAAAAAA
 AAAAAAATAA AAAAAGATCT TTAATTAAGC GGCCGCAAGC TTATTCCTCT
 TAGTGAG

FIGURE 2A

MARRLWILSL LAVTLTVALA APSQKSKRRT SSDRMKQIED KIEEILSKIY
 HIENEIARIK KLIGERTRSG NSSQNSRNKR AVQGPEETVT QDCLQLIADS
 ETPTIQKGSY TFVPWLLSFK RGSAALEKEN KILVKETGYF FIYGQVLYTD
 KTYAMGHLIQ RKKVHVFGDE LSLVTLFRCI QNMPETLPNN SCYSAGIAKL
 EEGDELQLAI PRENAQISLD GDVTFFGALK LL
 (SEQ ID NO:3)

FIGURE 3

200710-1955560

200710-1955360

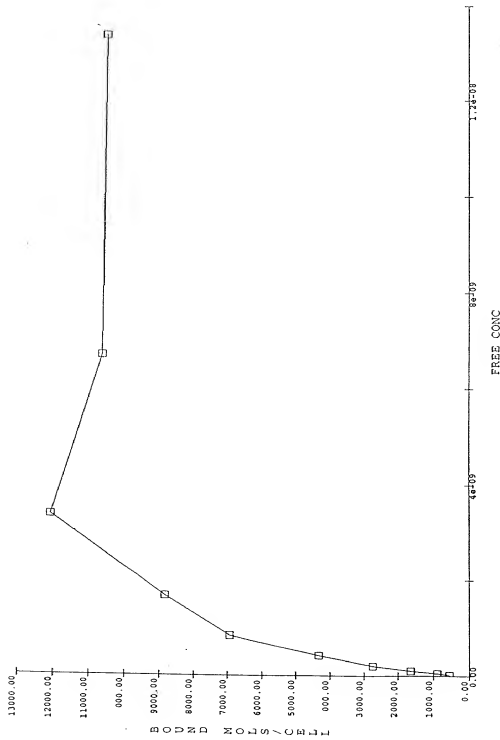


Figure 4A

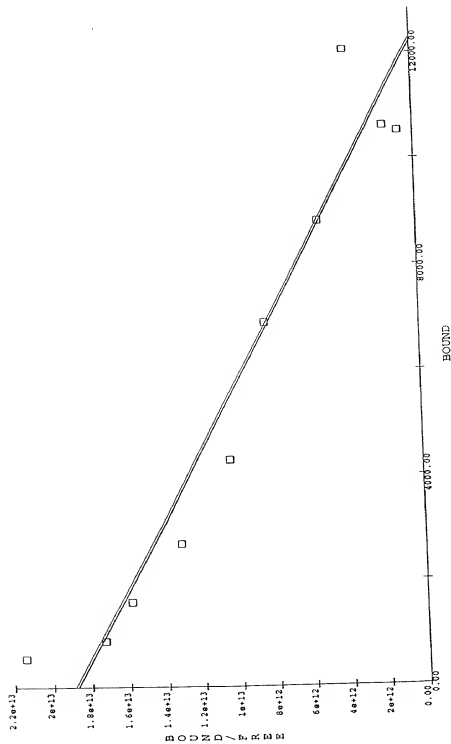


Figure 4B

20011019555860

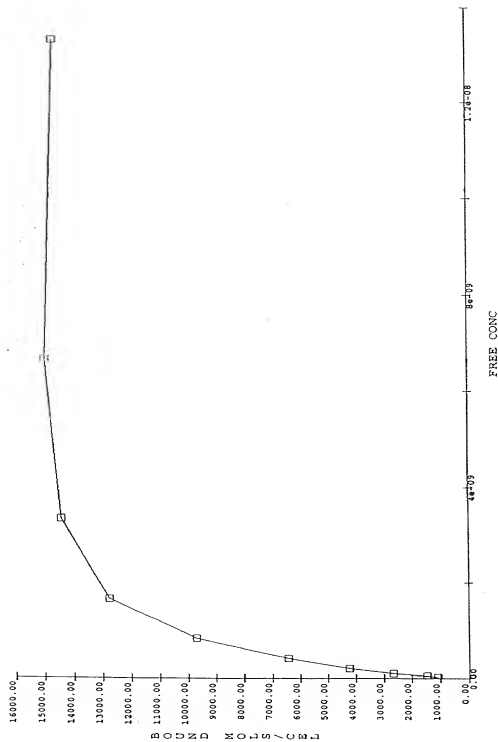


Figure 5A

200710-19555860

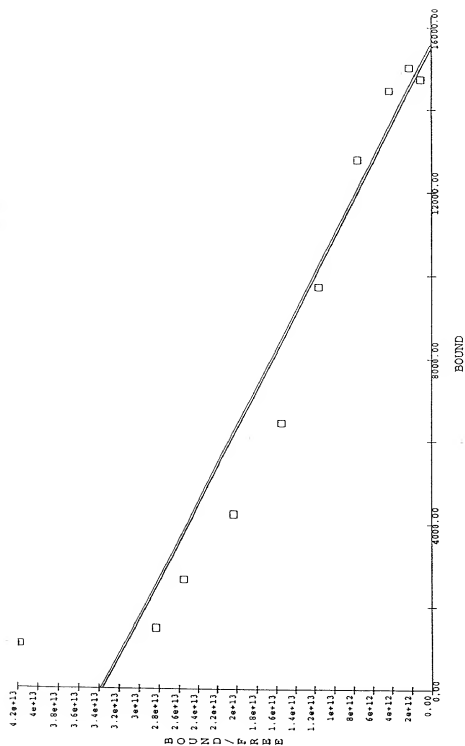


Figure 5B

20071107 19555660

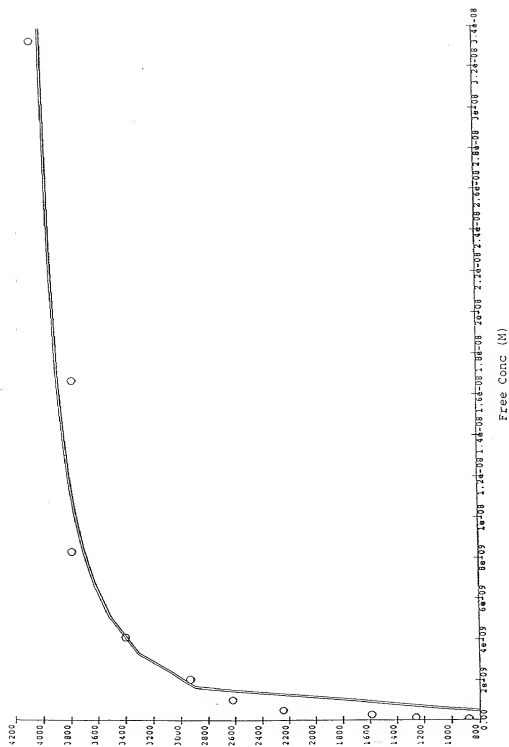


Figure 6A

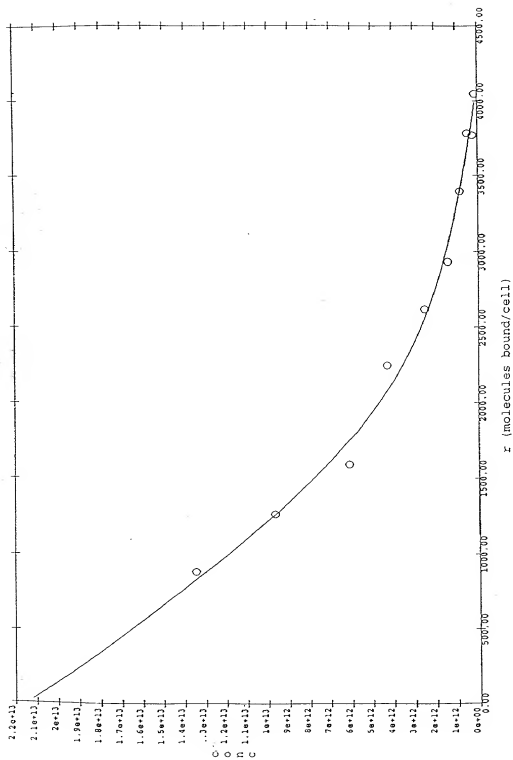


Figure 6B